

## SEQUENCE LISTING

<110> Lowery, David E.

Smith, Valdin G.

Kubiak, Teresa M.

Larsen, Martha J.

<120> Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods Related To  
The Same

<130> PHRM0002-103

Earlier Applications

<150> PriorAppNumber : US 10/283,423

<151> PriorFilingDate : 2002-10-30

<150> PriorAppNumber : 09/693,746

<151> PriorFilingDate : 2000-10-20

<150> PriorAppNumber : 09/425,676

<151> PriorFilingDate : 1999-10-22

<160> 187

<170> PatentIn version 3.2

<210> 1

<211> 1803

<212> DNA

<213> D. melanogaster

<400> 1  
atggccaact taagctggct gagcaccatc accaccacct cctcctccat cagcaccagc 60

cagctgccat tggtcagcac aaccaactgg agcctaacgt cgccgggaac tactagcgct 120  
atcttggcgg atgtggctgc atcggatgag gataggagcg gcgggatcat tcacaaccag 180  
ttcgtgcaaa tcttcttcta cgtcctgtac gccacgggtct ttgtcctggg tgtcttcgga 240  
aatgtcctgg tttgctacgt agttctgagg aatcggggcca tgcagactgt gaccaatata 300  
ttcatcacga atctggccct gtcggacata ttgctctgcg tcctggcggt gccatttact 360  
ccgctttaca cgttcatggg tcgctggggc ttcggcagga gtctgtgcca tctggtgtcc 420  
tttggccagg gatgcagcat ctacatatcc acgtgaccc tcacctcgat tgccatcgat 480  
cggtacttcg ttatcatata ccccttccat ccgcgcatga agctctccac ctgcatcggg 540  
atcatagtga gcatctgggt gatagccctg ctggccaccg ttccctacgg catgtacatg 600  
aagatgacca acgagctggt gaacggaacg cagacaggca acgagaccct ggtggaggcc 660  
actctaatagc taaacggaag ctttgtggcc cagggatcag gattcatcga ggcgccggac 720  
tctacctcgg ccaccaggc ctatatgcag gtgatgaccg ccggatcaac gggaccggag 780  
atgccctatg tgcgggtgta ctgcgaggag aactggccat cggagcagta ccggaagggtg 840  
ttcggtgcca tcacaaccac tctgcagttt gtgctgccct tcttcatcat ctcgatttgc 900  
tacgtgtgga tatcggtgaa gctaaaccag cgggccaggg ccaagccggg atcgaaatcc 960  
tcgagacggg aggaggcgga tcgggatcgc aagaagcgca ccaaccgcat gctcatcgcc 1020  
atggtggcgg tattcggact cagctggctg cccatcaatg tggtaacat attcgatgac 1080  
ttcgatgaca agtccaacga gtggcgcttc tacatcctat tcttctttgt ggccactct 1140  
attgccatga gctccacctg ctacaatccc ttctgtacg cctggctgaa cgagaacttc 1200  
cgcaaggagt tcaagcacgt gctgcctgc ttaataccct cgaacaaca catcatcaac 1260  
atcaccaggg gctataatcg gagtgatcgg aacacctgtg gtccgcgact gcatcatggc 1320  
aaggggggatg gtggcatggg cggtggcagt ctggacgccg acgaccagga cgagaacggc 1380  
atcaccagg agacctgtct gcccaaggag aagctgctga ttatccccag ggagccgact 1440  
tacggcaatg gcacgggtgc cgtgtcgcca atccttagcg ggcgcggcat taacgccgcc 1500  
ctggtgcacg gtggcgacca tcagatgcac cagctgcagc cgtcacacca tcaacagggtg 1560  
gagctgacga ggcgaatccg ccggcggaca gacgagacgg acggggatta cctggactcc 1620  
ggcgacgagc agaccgtgga ggtgcgcttc agcgagacgc cgttcgtcag cacggataat 1680  
accaccggga tcagcattct ggagacgagt acgagtcact gccaggactc ggatgtgatg 1740  
gtcgagctgg gcgaggcaat cggcgccggt ggtggggcag agctggggag gcgaatcaac 1800  
tga 1803

&lt;210&gt; 2

&lt;211&gt; 600

&lt;212&gt; PRT

&lt;213&gt; D. melanogaster

&lt;400&gt; 2

Met Ala Asn Leu Ser Trp Leu Ser Thr Ile Thr Thr Thr Ser Ser Ser  
 1 5 10 15

Ile Ser Thr Ser Gln Leu Pro Leu Val Ser Thr Thr Asn Trp Ser Leu  
 20 25 30

Thr Ser Pro Gly Thr Thr Ser Ala Ile Leu Ala Asp Val Ala Ala Ser  
 35 40 45

Asp Glu Asp Arg Ser Gly Gly Ile Ile His Asn Gln Phe Val Gln Ile  
 50 55 60

Phe Phe Tyr Val Leu Tyr Ala Thr Val Phe Val Leu Gly Val Phe Gly  
 65 70 75 80

Asn Val Leu Val Cys Tyr Val Val Leu Arg Asn Arg Ala Met Gln Thr  
 85 90 95

Val Thr Asn Ile Phe Ile Thr Asn Leu Ala Leu Ser Asp Ile Leu Leu  
 100 105 110

Cys Val Leu Ala Val Pro Phe Thr Pro Leu Tyr Thr Phe Met Gly Arg  
 115 120 125

Trp Ala Phe Gly Arg Ser Leu Cys His Leu Val Ser Phe Ala Gln Gly  
 130 135 140

Cys Ser Ile Tyr Ile Ser Thr Leu Thr Leu Thr Ser Ile Ala Ile Asp  
 145 150 155 160

Arg Tyr Phe Val Ile Ile Tyr Pro Phe His Pro Arg Met Lys Leu Ser  
 165 170 175

Thr Cys Ile Gly Ile Ile Val Ser Ile Trp Val Ile Ala Leu Leu Ala  
 180 185 190

Thr Val Pro Tyr Gly Met Tyr Met Lys Met Thr Asn Glu Leu Val Asn  
 195 200 205

Gly Thr Gln Thr Gly Asn Glu Thr Leu Val Glu Ala Thr Leu Met Leu  
 210 215 220

Asn Gly Ser Phe Val Ala Gln Gly Ser Gly Phe Ile Glu Ala Pro Asp  
 225 230 235 240

Ser Thr Ser Ala Thr Gln Ala Tyr Met Gln Val Met Thr Ala Gly Ser  
 245 250 255

Thr Gly Pro Glu Met Pro Tyr Val Arg Val Tyr Cys Glu Glu Asn Trp  
 260 265 270

Pro Ser Glu Gln Tyr Arg Lys Val Phe Gly Ala Ile Thr Thr Thr Leu  
 275 280 285

Gln Phe Val Leu Pro Phe Phe Ile Ile Ser Ile Cys Tyr Val Trp Ile  
 290 295 300

Ser Val Lys Leu Asn Gln Arg Ala Arg Ala Lys Pro Gly Ser Lys Ser  
 305 310 315 320

Ser Arg Arg Glu Glu Ala Asp Arg Asp Arg Lys Lys Arg Thr Asn Arg  
 325 330 335

Met Leu Ile Ala Met Val Ala Val Phe Gly Leu Ser Trp Leu Pro Ile  
 340 345 350

Asn Val Val Asn Ile Phe Asp Asp Phe Asp Asp Lys Ser Asn Glu Trp  
 355 360 365

Arg Phe Tyr Ile Leu Phe Phe Phe Val Ala His Ser Ile Ala Met Ser  
 370 375 380

Ser Thr Cys Tyr Asn Pro Phe Leu Tyr Ala Trp Leu Asn Glu Asn Phe  
 385 390 395 400

Arg Lys Glu Phe Lys His Val Leu Pro Cys Phe Asn Pro Ser Asn Asn  
 405 410 415

Asn Ile Ile Asn Ile Thr Arg Gly Tyr Asn Arg Ser Asp Arg Asn Thr  
 420 425 430

Cys Gly Pro Arg Leu His His Gly Lys Gly Asp Gly Gly Met Gly Gly  
 435 440 445  
 Gly Ser Leu Asp Ala Asp Asp Gln Asp Glu Asn Gly Ile Thr Gln Glu  
 450 455 460  
 Thr Cys Leu Pro Lys Glu Lys Leu Leu Ile Ile Pro Arg Glu Pro Thr  
 465 470 475 480  
 Tyr Gly Asn Gly Thr Gly Ala Val Ser Pro Ile Leu Ser Gly Arg Gly  
 485 490 495  
 Ile Asn Ala Ala Leu Val His Gly Gly Asp His Gln Met His Gln Leu  
 500 505 510  
 Gln Pro Ser His His Gln Gln Val Glu Leu Thr Arg Arg Ile Arg Arg  
 515 520 525  
 Arg Thr Asp Glu Thr Asp Gly Asp Tyr Leu Asp Ser Gly Asp Glu Gln  
 530 535 540  
 Thr Val Glu Val Arg Phe Ser Glu Thr Pro Phe Val Ser Thr Asp Asn  
 545 550 555 560  
 Thr Thr Gly Ile Ser Ile Leu Glu Thr Ser Thr Ser His Cys Gln Asp  
 565 570 575  
 Ser Asp Val Met Val Glu Leu Gly Glu Ala Ile Gly Ala Gly Gly Gly  
 580 585 590  
 Ala Glu Leu Gly Arg Arg Ile Asn  
 595 600

&lt;210&gt; 3

&lt;211&gt; 1445

&lt;212&gt; DNA

&lt;213&gt; D. melanogaster

&lt;400&gt; 3

atgaatcaga cggagcccgcc ccagctggca gatggggagc atctgagtgg atacgccagc 60

agcagcaaca gcgtgcgcta tctggacgac cggcatccgc tggactacct tgacctgggc 120

```

acggtgcacg ccctcaacac cactgccatc aacacctcgg atctgaatga gactgggagc 180
aggccgctgg acccggtgct tatcgatagg ttcttgagca acagggcggg ggacagcccc 240
tggtaccaca tgctcatcag catgtacggc gtgctaatacg tcttcggcgc ctaggcaac 300
accctggttg ttatagccgt catccggaag cccatcatgc gcactgctcg caatctgttc 360
atcctcaacc tggccatata ggacctactt ttatgcctag tcaccatgcc gctgaccttg 420
atggagatcc tgtccaagta ctggccctac ggctcctgct ccatcctgtg caaaacgatt 480
gccatgctgc aggcactttg tattttcgtg tcgacaatat ccataacggc cattgccttc 540
gacagatata aggtgatcgt gtacccacag cgggacagcc tgcagttcgt gggcgcggtg 600
acgatcctgg cggggatctg ggcaactggc ctgctgctgg cctcgccgct gttcgtctac 660
aaggagctga tcaacacaga cagccgggca ctctgcagc agatcggcct gcaggacacg 720
atcccgtact gcattgagga ctggccaagt cgcaacgggc gcttctacta ctgatcttc 780
tcgctgtgcg tacaatacct ggtgcccatc ctgatcgtct cgggtggcata cttcgggac 840
tacaacaagc tgaagagccg catcacctg gtggctgtgc aggcgtcctc cgctcagcgg 900
aaggtggagc gggggcggcg gatgaagcgc accaactgcc tactgatcag catcgccatc 960
atctttggcg tttcttggct gccgctgaac tttttcaacc tgtacgcgga catggagcgc 1020
tcgccggtca ctcagagcat gctagtccgc tacgccatct gccacatgat cggcatgagc 1080
tccgcctgct ccaaccogtt gctctacggc tggctcaacg acaacttccg taaagaattt 1140
caagaactgc tctgccgttg ctcagacact aatgttgctc ttaacggta cacgacaggc 1200
tgcaacgtcc aggcggcggc gcgcaagcgt cgcaagttgg gcgccgaact ctccaaaggc 1260
gaactcaagc tgctggggcc aggcggcgcc cagagcggta ccgccggcgg ggaaggcggg 1320
ctggcgccca ccgacttcat gaccggccac cacgagggcg gactgocgag cgccataacc 1380
gagtcggtgg ccctcacgga ccacaacccc gtgccctcgg aggtcaccaa gctgatgccg 1440
cggtg 1445

```

&lt;210&gt; 4

&lt;211&gt; 357

&lt;212&gt; PRT

&lt;213&gt; D. melanogaster

&lt;400&gt; 4

Met Glu Asn Thr Thr Met Leu Ala Asn Ile Ser Leu Asn Ala Thr Arg

1	5	10	15
Asn Glu Glu Asn Ile Thr Ser Phe Phe Thr Asp Glu Glu Trp Leu Ala	20	25	30
Ile Asn Gly Thr Leu Pro Trp Ile Val Gly Phe Phe Phe Gly Val Ile	35	40	45
Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val	50	55	60
Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu	65	70	75
Ala Ala Ala Asp Leu Met Phe Val Ile Leu Cys Ile Pro Phe Thr Ala	85	90	95
Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg	100	105	110
Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr	115	120	125
Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile	130	135	140
Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val	145	150	155
Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr	165	170	175
His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly	180	185	190
Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln	195	200	205
Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser	210	215	220
Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly	225	230	235
Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg			

245

250

255

Leu Val Val Val Val Val Ile Ala Phe Ala Ser Leu Trp Leu Pro Val  
 260 265 270

Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr  
 275 280 285

Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser  
 290 295 300

Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe  
 305 310 315 320

Arg Lys Ala Phe Tyr Lys Ala Val Asn Cys Ser Ser Arg Tyr Gln Asn  
 325 330 335

Tyr Thr Ser Asp Leu Pro Pro Pro Arg Lys Thr Ser Cys Ala Arg Thr  
 340 345 350

Ser Thr Thr Gly Leu  
 355

<210> 5

<211> 1376

<212> DNA

<213> D. melanogaster

<400> 5  
 atgaatcaga cggagcccg cccagctggca gatggggagc atctgagtgg atacgccagc 60  
 agcagcaaca gcgtgcgcta tctggacgac cggcatccgc tggactacct tgacctgggc 120  
 acggtgcacg ccctcaacac cactgccatc aacacctcgg atctgaatga gactgggagc 180  
 aggccgctgg acccggtgct tatcgatagg ttcttgagca acagggcggt ggacagcccc 240  
 tggataccaca tgctcatcag catgtacggc gtgctaatacgt tcttcggcgc cctaggcaac 300  
 accctgggtg ttatagccgt catccggaag cccatcatgc gcaactgctcg caatctgttc 360  
 atcctcaacc tggccatata ggacctactt ttatgcctag tcaccatgcc gctgaccttg 420  
 atggagatcc tgtccaagta ctggccctac ggctcctgct ccattcctgtg caaaacgatt 480  
 gccatgctgc aggcactttg tattttcgtg tcgacaatat ccataacggc cattgccttc 540



gacagatattc aggtgatcgt gtacccccacg cgggacagcc tgcagttcgt gggcgcggtg 600  
 acgatcctgg cggggatctg ggcactggca ctgctgctgg cctcgccgct gttcgtctac 660  
 aaggagctga tcaacacaga cacgccggca ctctgcagc agatcggcct gcaggacacg 720  
 atcccgtact gcattgagga ctggccaagt cgcaacgggc gcttctacta ctgatcttc 780  
 tcgctgtgcg tacaatacct ggtgcccata ctgatcgtct cggtggcata cttcgggata 840  
 tacaacaagc tgaagagccg catcacctg gtggctgtgc aggcgtcctc cgctcagcgg 900  
 aaggtggagc gggggcggcg gatgaagcgc accaactgcc tactgatcag catcgccatc 960  
 atctttggcg tttcttggtt gccgctgaac ttttcaacc tgtacgcgga catggagcgc 1020  
 tcgccggtca ctcagagcat gctagtccgc tacgccatct gccacatgat cggcatgagc 1080  
 tccgcctgct ccaacccggt gctctacggc tggctcaacg acaacttccg ctgcaacgctc 1140  
 caggcggcgg cgcgcaagcg tcgcaagttg ggcgcgaac tctccaaagg cgaactcaag 1200  
 ctgctggggc caggcggcgc ccagagcggg accgccggcg gggaaggcgg tctggcggcc 1260  
 accgacttca tgaccggcca ccacgagggc ggactgcgca gcgccataac cgagtcggtg 1320  
 gccctcacgg accacaaccc cgtgccctcg gaggtcacca agctgatgcc gcggtg 1376

<210> 6

<211> 458

<212> PRT

<213> D. melanogaster

<400> 6

Met Asn Gln Thr Glu Pro Ala Gln Leu Ala Asp Gly Glu His Leu Ser  
1 5 10 15

Gly Tyr Ala Ser Ser Ser Asn Ser Val Arg Tyr Leu Asp Asp Arg His  
20 25 30

Pro Leu Asp Tyr Leu Asp Leu Gly Thr Val His Ala Leu Asn Thr Thr  
35 40 45

Ala Ile Asn Thr Ser Asp Leu Asn Glu Thr Gly Ser Arg Pro Leu Asp  
50 55 60

Pro Val Leu Ile Asp Arg Phe Leu Ser Asn Arg Ala Val Asp Ser Pro  
65 70 75 80

Trp Tyr His Met Leu Ile Ser Met Tyr Gly Val Leu Ile Val Phe Gly  
 85 90 95

Ala Leu Gly Asn Thr Leu Val Val Ile Ala Val Ile Arg Lys Pro Ile  
 100 105 110

Met Arg Thr Ala Arg Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp  
 115 120 125

Leu Leu Leu Cys Leu Val Thr Met Pro Leu Thr Leu Met Glu Ile Leu  
 130 135 140

Ser Lys Tyr Trp Pro Tyr Gly Ser Cys Ser Ile Leu Cys Lys Thr Ile  
 145 150 155 160

Ala Met Leu Gln Ala Leu Cys Ile Phe Val Ser Thr Ile Ser Ile Thr  
 165 170 175

Ala Ile Ala Phe Asp Arg Tyr Gln Val Ile Val Tyr Pro Thr Arg Asp  
 180 185 190

Ser Leu Gln Phe Val Gly Ala Val Thr Ile Leu Ala Gly Ile Trp Ala  
 195 200 205

Leu Ala Leu Leu Leu Ala Ser Pro Leu Phe Val Tyr Lys Glu Leu Ile  
 210 215 220

Asn Thr Asp Thr Pro Ala Leu Leu Gln Gln Ile Gly Leu Gln Asp Thr  
 225 230 235 240

Ile Pro Tyr Cys Ile Glu Asp Trp Pro Ser Arg Asn Gly Arg Phe Tyr  
 245 250 255

Tyr Ser Ile Phe Ser Leu Cys Val Gln Tyr Leu Val Pro Ile Leu Ile  
 260 265 270

Val Ser Val Ala Tyr Phe Gly Ile Tyr Asn Lys Leu Lys Ser Arg Ile  
 275 280 285

Thr Val Val Ala Val Gln Ala Ser Ser Ala Gln Arg Lys Val Glu Arg  
 290 295 300

Gly Arg Arg Met Lys Arg Thr Asn Cys Leu Leu Ile Ser Ile Ala Ile  
 305 310 315 320

Ile Phe Gly Val Ser Trp Leu Pro Leu Asn Phe Phe Asn Leu Tyr Ala  
                   325                                  330                                  335

Asp Met Glu Arg Ser Pro Val Thr Gln Ser Met Leu Val Arg Tyr Ala  
                   340                                  345                                  350

Ile Cys His Met Ile Gly Met Ser Ser Ala Cys Ser Asn Pro Leu Leu  
                   355                                  360                                  365

Tyr Gly Trp Leu Asn Asp Asn Phe Arg Cys Asn Val Gln Ala Ala Ala  
                   370                                  375                                  380

Arg Lys Arg Arg Lys Leu Gly Ala Glu Leu Ser Lys Gly Glu Leu Lys  
                   385                                  390                                  395                                  400

Leu Leu Gly Pro Gly Gly Ala Gln Ser Gly Thr Ala Gly Gly Glu Gly  
                                   405                                  410                                  415

Gly Leu Ala Ala Thr Asp Phe Met Thr Gly His His Glu Gly Gly Leu  
                                   420                                  425                                  430

Arg Ser Ala Ile Thr Glu Ser Val Ala Leu Thr Asp His Asn Pro Val  
                   435                                  440                                  445

Pro Ser Glu Val Thr Lys Leu Met Pro Arg  
                   450                                  455

<210> 7

<211> 1073

<212> DNA

<213> D. melanogaster

<400> 7  
 atggagaaca ccacaatgct ggctaataatt agcctaaatg caaccagaaa tgaggagaat 60  
 atcacctcat tcttcaccga cgaagagtgg ctggccatca atggcacttt gccgtggata 120  
 gtgggattct tcttcggcgt catcgccatc acgggattct tcggcaacct gctggatcatc 180  
 ctggtggtgg tcttcaacaa caacatgcgc tccaccacca acctgatgat tgtcaatctg 240  
 gctgccgctg atctgatgtt cgtaatcctc tgcattccct tcacggccac cgattacatg 300  
 gtgtactact ggccatatgg aaggttctgg tgccgcagtg tccagtacct gattgtggtg 360

accgccttcg cctccatcta cacgctggtg ctaatgtcca tcgatcggtt cctggcgggtg 420  
 gttcatccca ttcgctcgcg gatgatgagg acggagaaca ttaccctgat tgccatcgtg 480  
 actctgtgga tcgtggtgct ggctgtttcg gtgccagtgg ccttcaccca cgacgtggtg 540  
 gtggactacg atgcaaagaa gaacatcacc tacggcatgt gcaccttcac gacgaacgac 600  
 ttccttggtc cgcgcacctt ccagggtcacc ttcttcatca gctcctacct gctgcccctg 660  
 atgatcatca gcggtctcta catgcgcatg atcatgcggc tctggcgcca gggaaccggc 720  
 gtccgcatgt ccaaggagtc gcagcgcggt cgcaagcggg tcacccgact cgtcgtcgtg 780  
 gtggtcatcg ccttcgcctc gctctggctg cctgtccagc tcctcctgct gctcaagtca 840  
 ctggatgtca tcgagacgaa caccctcacc aagctagtca tccagggtcac cgcccagact 900  
 ctggcctaca gcagctcgtg tatcaatccg ctgctctacg ccttcctctc cgagaatttc 960  
 cggaaggcct tctataaggc cgtaactgc tcctctcgat accagaacta cacatctgat 1020  
 ttgccgccgc cgcgcaagac gtcctgtgcc aggacctcca ccactggact cta 1073

<210> 8

<211> 357

<212> PRT

<213> D. melanogaster

<400> 8

Met Glu Asn Thr Thr Met Leu Ala Asn Ile Ser Leu Asn Ala Thr Arg  
1 5 10 15

Asn Glu Glu Asn Ile Thr Ser Phe Phe Thr Asp Glu Glu Trp Leu Ala  
20 25 30

Ile Asn Gly Thr Leu Pro Trp Ile Val Gly Phe Phe Phe Gly Val Ile  
35 40 45

Ala Ile Thr Gly Phe Phe Gly Asn Leu Leu Val Ile Leu Val Val Val  
50 55 60

Phe Asn Asn Asn Met Arg Ser Thr Thr Asn Leu Met Ile Val Asn Leu  
65 70 75 80

Ala Ala Ala Asp Leu Met Phe Val Ile Leu Cys Ile Pro Phe Thr Ala  
85 90 95

Thr Asp Tyr Met Val Tyr Tyr Trp Pro Tyr Gly Arg Phe Trp Cys Arg  
 100 105 110

Ser Val Gln Tyr Leu Ile Val Val Thr Ala Phe Ala Ser Ile Tyr Thr  
 115 120 125

Leu Val Leu Met Ser Ile Asp Arg Phe Leu Ala Val Val His Pro Ile  
 130 135 140

Arg Ser Arg Met Met Arg Thr Glu Asn Ile Thr Leu Ile Ala Ile Val  
 145 150 155 160

Thr Leu Trp Ile Val Val Leu Val Val Ser Val Pro Val Ala Phe Thr  
 165 170 175

His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly  
 180 185 190

Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln  
 195 200 205

Val Thr Phe Phe Ile Ser Ser Tyr Leu Leu Pro Leu Met Ile Ile Ser  
 210 215 220

Gly Leu Tyr Met Arg Met Ile Met Arg Leu Trp Arg Gln Gly Thr Gly  
 225 230 235 240

Val Arg Met Ser Lys Glu Ser Gln Arg Gly Arg Lys Arg Val Thr Arg  
 245 250 255

Leu Val Val Val Val Val Ile Ala Phe Ala Ser Leu Trp Leu Pro Val  
 260 265 270

Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr  
 275 280 285

Leu Thr Lys Leu Val Ile Gln Val Thr Ala Gln Thr Leu Ala Tyr Ser  
 290 295 300

Ser Ser Cys Ile Asn Pro Leu Leu Tyr Ala Phe Leu Ser Glu Asn Phe  
 305 310 315 320

Arg Lys Ala Phe Tyr Lys Ala Val Asn Cys Ser Ser Arg Tyr Gln Asn  
 325 330 335

Tyr Thr Ser Asp Leu Pro Pro Pro Arg Lys Thr Ser Cys Ala Arg Thr  
 340 345 350

Ser Thr Thr Gly Leu  
 355

<210> 9

<211> 1559

<212> DNA

<213> D. melanogaster

<400> 9

```

atggagaatc gcagtgaact cgaggcggat gactacggcg acatcagttg gagcaattgg      60
agcaactgga gcacccccgc cggcggtcctt ttctcggcca tgagcagcgt gctctcggcc      120
agcaaccata cgccctgcc ggactttggc caggagctcg ccctatccac cagctccttc      180
aatcacagcc agaccctatc caccgaccag cccgccgtcg gggacgtgga agacgcggcc      240
gaggatgcgg cggcggtccat ggagacgggc tcgtttgcat ttgtgggtccc gtggtggcgt      300
cagggtgctct ggagcatcct cttcggcggc atggtcattg tggcgacggg cggtaacctg      360
attgttgtct ggatcgtgat gacgaccaag cggatgcgga cggtaaccaa ctatttcata      420
gtgaatctct ccatcgcgga cgccatgggtg tccagcctaa acgtcacctt caactactac      480
tatatgctgg atagcgactg gcccttcggc gagtttact gcaagttgtc ccagttcatc      540
gcgatgctaa gcatctgcgc ctcaagtgtc accctaattg ccatctccat cgacagatac      600
gtggccatca tccggccact gcagccgcgg atgagcaagc ggtgcaacct ggccatcgcg      660
gcgggtcatct ggctggcctc cacgctcatc tcctgcccc tgatgatcat ctaccgcacg      720
gaggaggtgc cggtcgcgg gctcagcaac cgcacggtct gctaccgga gtggcccgat      780
gggcccacca atcaactcac gatggagtcc ctctacaaca tcctcatcat catyctaacc      840
tacttcctgc ccatcgtctc catgacggtc acctactcgc gcgtgggcat cgagctctgg      900
ggatccaaga ccatcggcga gtgcacgccc cgccaggtgg araaygtgcg gagtaagcga      960
agggtggtga agatgatgat tgtgggtcgtc ctgatattcg ccatctgctg gctgccgttc     1020
cacagctact tcataatcac atcctgctac ccggccatca cggaggcgcc cttcatccag     1080
gaactctacc tggccatcta ctggctggcc atgagcaact ccatgtacaa tccattata     1140
tactgctgga tgaattcgcg ctttcgctat ggtttcaaga tggctcttcg ctgggtgcctg     1200

```

tttgtgcgcg tgggcactga accctttagt cggcgggaga acctgacatc cgggtactcc 1260  
 tgctccggtt ccccgatca caatcgcac aagcgcaatg ataccagaa atcgatactt 1320  
 tatacctgtc ccagctcacc caagtcgcat cgaatttcgc acagcggaac aggtcgcagt 1380  
 gcgacgctgc ggaacagtct gccggcggag tctactgtcg cggcgggatc tgggtggtgga 1440  
 gggcacagga aacggttgct ctaccagcag gaaatgcagc agcggttggtc aggacccaat 1500  
 agtgccaccg cagtgaacaa ttccagcagt acggccaaca ccaccaact gctctcctg 1559

<210> 10

<211> 519

<212> PRT

<213> D. melanogaster

<400> 10

Met Glu Asn Arg Ser Asp Phe Glu Ala Asp Asp Tyr Gly Asp Ile Ser  
 1 5 10 15

Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val Leu Phe Ser  
 20 25 30

Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro Leu Pro Asp  
 35 40 45

Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn His Ser Gln  
 50 55 60

Thr Leu Ser Thr Asp Gln Pro Ala Val Gly Asp Val Glu Asp Ala Ala  
 65 70 75 80

Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala Phe Val Val  
 85 90 95

Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly Gly Met Val  
 100 105 110

Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile Val Met Thr  
 115 120 125

Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ser  
 130 135 140

Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe Asn Tyr Tyr  
 145 150 155 160

Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr Cys Lys Leu  
 165 170 175

Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val Phe Thr Leu  
 180 185 190

Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg Pro Leu Gln  
 195 200 205

Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala Val Ile Trp  
 210 215 220

Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile Tyr Arg Thr  
 225 230 235 240

Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val Cys Tyr Pro  
 245 250 255

Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu Ser Leu Tyr  
 260 265 270

Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile Val Ser Met  
 275 280 285

Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly Ser Lys Thr  
 290 295 300

Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg Ser Lys Arg  
 305 310 315 320

Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe Ala Ile Cys  
 325 330 335

Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys Tyr Pro Ala  
 340 345 350

Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala Ile Tyr Trp  
 355 360 365

Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr Cys Trp Met  
 370 375 380



Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg Trp Cys Leu  
 385 390 395 400

Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu Asn Leu Thr  
 405 410 415

Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg Ile Lys Arg  
 420 425 430

Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser Ser Pro Lys  
 435 440 445

Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala Thr Leu Arg  
 450 455 460

Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser Gly Gly Gly  
 465 470 475 480

Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln Gln Arg Trp  
 485 490 495

Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser Ser Thr Ala  
 500 505 510

Asn Thr Thr Gln Leu Leu Ser  
 515

<210> 11

<211> 1568

<212> DNA

<213> D. melanogaster

<400> 11  
 atggagaatc gcagtgaactt cgaggoggat gactacggcg acatcagttg gagcaattgg 60  
 agcaattgga gcaactggag caccocccgcc ggcgtccttt tctcggccat gagcagcgtg 120  
 ctctcggcca gcaaccatac gcctctgccg gactttggcc aggagctcgc cctatccacc 180  
 agctccttca atcacagcca gaccctatcc accgacctgc cgcgcgtcgg ggacgtggaa 240  
 gacgcggccg aggatgcggc ggcgtccatg gagacgggct cgtttgcatt tgtggtcccc 300  
 tggtggcgctc aggtgctctg gagcctcctc ttcggcgcca tggtcattgt ggcgacgggc 360

ggtaacctga ttgttgtctg gatcgtgatg acgaccaagc ggatgcggac ggtaaccaac 420  
 tatttcatag taaatctctc catcgcggac gccatggtgt ccagcctgaa cgtcaccttc 480  
 aactactact acatgctgga tagcgactgg cccttcggcg agttctactg caagttgtcc 540  
 cagttcatcg cgatgctaag catctgcgcc tcagtgttca ccctaattggc catctccatc 600  
 gacagatacg tggccatcat cgggccactg cagccgcgga tgagcaagcg gtgcaacctg 660  
 gccatcgcgg cggtcatctg gctggcctcc acgctcatct cctgccccat gatgatcatc 720  
 taccgcacgg aggaggtgcc ggtccgcggg ctacgcaacc gcacgggtctg ctaccgggag 780  
 tggcccgatg ggcccaccaa tcaactccacg atggagtccc tctacaacat cctcatcatc 840  
 attctaacct acttctctgcc catcgtctcc atgacgggtca cctactcgcg cgtgggcatc 900  
 gagctctggg gatccaagac catcggcgag tgcacgcccc gccaggtgga gaatgtgcgg 960  
 agtaagcgaa ggggtggtgaa gatgatgatt gtggtcgtcc tgatattcgc catctgctgg 1020  
 ctgccgttcc acagctactt cataatcaca tcctgctacc cggccatcac ggaggcgccc 1080  
 ttcattccagg aactttacct ggccatctac tggctggcca tgagcaactc catgtacaat 1140  
 cccattatat actgctggat gaattcgcgc ttctgctatg gtttcaagat ggtcttccgc 1200  
 tggtgcctgt ttgtgcgcgt gggcactgaa cccttttagtc ggcgggagaa cctgacatcc 1260  
 cggtaactct gctccgggttc cccggatcac aatcgcatca agcgcaatga taccagaaa 1320  
 tcgatacttt atacctgtcc cagctcacc aagtcgcatc gaatttcgca cagcggaaca 1380  
 ggtcgcagtg cgacgctgag gaacagtctg ccggcggagt cattgtcgtc cgggtggatct 1440  
 ggaggtggag gacacaggaa acggttgtcc taccagcagg aaatgcagca gcggtggtca 1500  
 ggacccaata gtgccaccgc agtgaccaat tccagcagta cggccaacac cacccaactg 1560  
 ctctcctg 1568

<210> 12

<211> 522

<212> PRT

<213> D. melanogaster

<400> 12

Met Glu Asn Arg Ser Asp Phe Glu Ala Asp Asp Tyr Gly Asp Ile Ser  
 1 5 10 15

Trp Ser Asn Trp Ser Asn Trp Ser Thr Pro Ala Gly Val

20

25

30

Leu Phe Ser Ala Met Ser Ser Val Leu Ser Ala Ser Asn His Thr Pro  
 35 40 45

Leu Pro Asp Phe Gly Gln Glu Leu Ala Leu Ser Thr Ser Ser Phe Asn  
 50 55 60

His Ser Gln Thr Leu Ser Thr Asp Leu Pro Ala Val Gly Asp Val Glu  
 65 70 75 80

Asp Ala Ala Glu Asp Ala Ala Ala Ser Met Glu Thr Gly Ser Phe Ala  
 85 90 95

Phe Val Val Pro Trp Trp Arg Gln Val Leu Trp Ser Ile Leu Phe Gly  
 100 105 110

Gly Met Val Ile Val Ala Thr Gly Gly Asn Leu Ile Val Val Trp Ile  
 115 120 125

Val Met Thr Thr Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Ile Val  
 130 135 140

Asn Leu Ser Ile Ala Asp Ala Met Val Ser Ser Leu Asn Val Thr Phe  
 145 150 155 160

Asn Tyr Tyr Tyr Met Leu Asp Ser Asp Trp Pro Phe Gly Glu Phe Tyr  
 165 170 175

Cys Lys Leu Ser Gln Phe Ile Ala Met Leu Ser Ile Cys Ala Ser Val  
 180 185 190

Phe Thr Leu Met Ala Ile Ser Ile Asp Arg Tyr Val Ala Ile Ile Arg  
 195 200 205

Pro Leu Gln Pro Arg Met Ser Lys Arg Cys Asn Leu Ala Ile Ala Ala  
 210 215 220

Val Ile Trp Leu Ala Ser Thr Leu Ile Ser Cys Pro Met Met Ile Ile  
 225 230 235 240

Tyr Arg Thr Glu Glu Val Pro Val Arg Gly Leu Ser Asn Arg Thr Val  
 245 250 255

Cys Tyr Pro Glu Trp Pro Asp Gly Pro Thr Asn His Ser Thr Met Glu

260

265

270

Ser Leu Tyr Asn Ile Leu Ile Ile Ile Leu Thr Tyr Phe Leu Pro Ile  
 275 280 285

Val Ser Met Thr Val Thr Tyr Ser Arg Val Gly Ile Glu Leu Trp Gly  
 290 295 300

Ser Lys Thr Ile Gly Glu Cys Thr Pro Arg Gln Val Glu Asn Val Arg  
 305 310 315 320

Ser Lys Arg Arg Val Val Lys Met Met Ile Val Val Val Leu Ile Phe  
 325 330 335

Ala Ile Cys Trp Leu Pro Phe His Ser Tyr Phe Ile Ile Thr Ser Cys  
 340 345 350

Tyr Pro Ala Ile Thr Glu Ala Pro Phe Ile Gln Glu Leu Tyr Leu Ala  
 355 360 365

Ile Tyr Trp Leu Ala Met Ser Asn Ser Met Tyr Asn Pro Ile Ile Tyr  
 370 375 380

Cys Trp Met Asn Ser Arg Phe Arg Tyr Gly Phe Lys Met Val Phe Arg  
 385 390 395 400

Trp Cys Leu Phe Val Arg Val Gly Thr Glu Pro Phe Ser Arg Arg Glu  
 405 410 415

Asn Leu Thr Ser Arg Tyr Ser Cys Ser Gly Ser Pro Asp His Asn Arg  
 420 425 430

Ile Lys Arg Asn Asp Thr Gln Lys Ser Ile Leu Tyr Thr Cys Pro Ser  
 435 440 445

Ser Pro Lys Ser His Arg Ile Ser His Ser Gly Thr Gly Arg Ser Ala  
 450 455 460

Thr Leu Arg Asn Ser Leu Pro Ala Glu Ser Leu Ser Ser Gly Gly Ser  
 465 470 475 480

Gly Gly Gly Gly His Arg Lys Arg Leu Ser Tyr Gln Gln Glu Met Gln  
 485 490 495

Gln Arg Trp Ser Gly Pro Asn Ser Ala Thr Ala Val Thr Asn Ser Ser

500

505

510

Ser Thr Ala Asn Thr Thr Gln Leu Leu Ser  
515 520

&lt;210&gt; 13

&lt;211&gt; 1394

&lt;212&gt; DNA

&lt;213&gt; D. melanogaster

&lt;400&gt; 13

```

atggagcacc acaatagcca tctgttgccct ggtggcagcg agaagatgta ctacatagct      60
caccagcagc cgatgctgcg gaacgaggat gataactacc aggaggggta cttcatcagg      120
ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaaggggtcc      180
aactatggat atggctccac cacaacgctc agtggcctcc agttcgagac ctataatatc      240
actgtgatga tgaacttttag ctgtgacgac tatgaccttc tatcggagga catgtggtct      300
agtgcctact ttaagatcat cgtctacatg ctctacattc ccatctttat ctctgccctg      360
atcggcaacg gaacgggtctg ctatatcgtc tattccacac ctgcgatgcg cacggtcacc      420
aattacttta tagccagctt ggccatcggc gacatcctga tgtccttctt ctgcgttccg      480
tcgtccttca tctcgtgtgt catcctgaac tactggcctt ttggcctggc cctctgtcac      540
tttgtgaact actcgcaggc ggtctcagtt ctggtcagcg cctatacttt ggtggcaatt      600
agcattgacc gctacatagc cattatgtgg ccattaaagc cacgcatcac aaaacgctat      660
gccaccttca tcatcgccgg cgtttggttt attgcaactg ccaccgcact tcccataccc      720
atcgtctctg gactcgacat cccaatgtcg ccgtggcaca cgaaatgca gaaatacatt      780
tgccgcgaaa tgtggccgct gcggacgcag gactactact acaccctgtc cctcttcgcg      840
ctgcagttcg tcgtgccgct gggcgtgctc atcttcacct acgcccggtat caccattcgc      900
gtctggggcg aacgaccgcc aggcgaggcg gaaaccaacc gcgaccagcg gatggcacgc      960
tccaaacgga agatgggtcaa aatgatgctg acggttgtga ttgtgttcac ctgctgttgg      1020
ctgcccttca atattttgca gcttttactg aacgacgagg agttcgccca ctgggatcct      1080
ctgccgtatg tatggttcgc gtttactggt ctggccatgt cgcaactgctg ctacaatccg      1140
atcatctact gctacatgaa cgcccgtttc aggagcggat tcgtccagct gatgcaccgt      1200
atgcccggcc tgcgtcgtg gtgctgctg cggagcgtcg gtgatcgcat gaacgcaact      1260

```

tccggaacgg gtccagcact tcctctcaat cgaatgaaca catccaccac ctacatcagc 1320  
 gctcgtcgaa agccacgagc gacatctttg cgagcgaacc cattatcatg cggcgagacg 1380  
 tcaccactgc ggta 1394

<210> 14

<211> 464

<212> PRT

<213> D. melanogaster

<400> 14

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met '  
 1 5 10 15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn  
 20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr  
 35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr  
 50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile  
 65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu  
 85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr  
 100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr  
 115 120 125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile  
 130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro  
 145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu

165

170

175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val  
 180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile  
 195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile  
 210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro  
 225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys  
 245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr  
 260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly  
 275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys  
 290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg  
 305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe  
 325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp  
 340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe  
 355 360 365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys  
 370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg  
 385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg

405

410

415

Met Asn Ala Thr Ser Gly Thr Gly Pro Ala Leu Pro Leu Asn Arg Met  
 420 425 430

Asn Thr Ser Thr Thr Tyr Ile Ser Ala Arg Arg Lys Pro Arg Ala Thr  
 435 440 445

Ser Leu Arg Ala Asn Pro Leu Ser Cys Gly Glu Thr Ser Pro Leu Arg  
 450 455 460

&lt;210&gt; 15

&lt;211&gt; 1556

&lt;212&gt; DNA

&lt;213&gt; D. melanogaster

<400> 15  
 atggagcacc acaatagcca tctgttgccct ggtggcagcg agaagatgta ctacatagct 60  
 caccagcagc cgatgctgcg gaacgaggat gataactacc aggaggggta cttcatcagg 120  
 ccggaccctg catccttact ttacaatacc accgcactgc cagcggacga tgaaggggtcc 180  
 aactatggat atgggtccac cacaacgctc agtggcctcc agttcgagac ctataatatc 240  
 actgtgatga tgaacttttag ctgtgacgac tatgaccttc tatcggagga catgtggtct 300  
 agtgccctact ttaagatcat cgtctacatg ctctacattc ccatctttat cttcgccctg 360  
 atcggcaacg gaacggctcg ctatatcgtc tattccacac ctgcgatgcg cacggtcacc 420  
 aattacttta tagccagctt ggccatcggc gacatcctga tgtccttctt ctgcgttcgg 480  
 tcgtccttca tctcgctggt catcctgaac tactggcctt ttggcctggc cctctgtcac 540  
 tttgtgaact actcgcaggc ggtctcagtt ctggtcagcg cctatacttt ggtggcaatt 600  
 agcattgacc gctacatagc cattatgtgg ccattaaagc cacgcatcac aaaacgctat 660  
 gccaccttca tcatcgccgg cgtttgggtt attgcacttg ccaccgcact tccataccc 720  
 atcgtctctg gactcgacat cccaatgtcg ccgtggcaca cgaaatgca gaaatacatt 780  
 tgccgcgaaa tgtggccgct gcggacgcag gactactact acaccctgtc cctcttcgcg 840  
 ctgcagttcg tcgtgccgct gggcgtgctc atcttcacct acgcccggat caccattcgc 900  
 gtctgggcca aacgaccgcc aggcgaggcg gaaaccaacc gcgaccagcg gatggcacgc 960  
 tccaaacgga agatgggtcaa aatgatgctg acggttgtga ttgtgttcac ctgctgttgg 1020



ctgcccttca atattttgca gcttttactg aacgacgagg agttcgccca ctgggacct 1080  
 ctgccgtatg tgtggttcgc gtttcaactgg ctggccatgt cgcactgctg ctacaatccg 1140  
 atcatctact gctacatgaa cgcccgtttc aggagcggat tcgtccagct gatgcaccgt 1200  
 atgcccgcc tgcgtcgctg gtgctgcctg cggagcgtcg gtgatcgcat gaacgcaact 1260  
 tccggtgaga tgactacgaa gtaccatcgc catgtcggcg atgccctatt ccggaaaccc 1320  
 aaaatatgca ttaggaacgg gtccagcact tcctctcaat cgaatgaaca catccaccac 1380  
 ctacatcagc gctcgtcgaa agccacgagc gacatctttg cgagcgaacc cattatcatg 1440  
 cggcgagacg tcaccactgc ggtagctgtc atatcaaaaa ataaaactga ttcaccggtg 1500  
 cgccgatcgg gaagctcagg tggaacagaa gcaaacataa gaagcaccga gttttg 1556

<210> 16

<211> 518

<212> PRT

<213> D. melanogaster

<400> 16

Met Glu His His Asn Ser His Leu Leu Pro Gly Gly Ser Glu Lys Met  
1 5 10 15

Tyr Tyr Ile Ala His Gln Gln Pro Met Leu Arg Asn Glu Asp Asp Asn  
20 25 30

Tyr Gln Glu Gly Tyr Phe Ile Arg Pro Asp Pro Ala Ser Leu Leu Tyr  
35 40 45

Asn Thr Thr Ala Leu Pro Ala Asp Asp Glu Gly Ser Asn Tyr Gly Tyr  
50 55 60

Gly Ser Thr Thr Thr Leu Ser Gly Leu Gln Phe Glu Thr Tyr Asn Ile  
65 70 75 80

Thr Val Met Met Asn Phe Ser Cys Asp Asp Tyr Asp Leu Leu Ser Glu  
85 90 95

Asp Met Trp Ser Ser Ala Tyr Phe Lys Ile Ile Val Tyr Met Leu Tyr  
100 105 110

Ile Pro Ile Phe Ile Phe Ala Leu Ile Gly Asn Gly Thr Val Cys Tyr

115

120

125

Ile Val Tyr Ser Thr Pro Arg Met Arg Thr Val Thr Asn Tyr Phe Ile  
 130 135 140

Ala Ser Leu Ala Ile Gly Asp Ile Leu Met Ser Phe Phe Cys Val Pro  
 145 150 155 160

Ser Ser Phe Ile Ser Leu Phe Ile Leu Asn Tyr Trp Pro Phe Gly Leu  
 165 170 175

Ala Leu Cys His Phe Val Asn Tyr Ser Gln Ala Val Ser Val Leu Val  
 180 185 190

Ser Ala Tyr Thr Leu Val Ala Ile Ser Ile Asp Arg Tyr Ile Ala Ile  
 195 200 205

Met Trp Pro Leu Lys Pro Arg Ile Thr Lys Arg Tyr Ala Thr Phe Ile  
 210 215 220

Ile Ala Gly Val Trp Phe Ile Ala Leu Ala Thr Ala Leu Pro Ile Pro  
 225 230 235 240

Ile Val Ser Gly Leu Asp Ile Pro Met Ser Pro Trp His Thr Lys Cys  
 245 250 255

Glu Lys Tyr Ile Cys Arg Glu Met Trp Pro Ser Arg Thr Gln Glu Tyr  
 260 265 270

Tyr Tyr Thr Leu Ser Leu Phe Ala Leu Gln Phe Val Val Pro Leu Gly  
 275 280 285

Val Leu Ile Phe Thr Tyr Ala Arg Ile Thr Ile Arg Val Trp Ala Lys  
 290 295 300

Arg Pro Pro Gly Glu Ala Glu Thr Asn Arg Asp Gln Arg Met Ala Arg  
 305 310 315 320

Ser Lys Arg Lys Met Val Lys Met Met Leu Thr Val Val Ile Val Phe  
 325 330 335

Thr Cys Cys Trp Leu Pro Phe Asn Ile Leu Gln Leu Leu Leu Asn Asp  
 340 345 350

Glu Glu Phe Ala His Trp Asp Pro Leu Pro Tyr Val Trp Phe Ala Phe

355

360

365

His Trp Leu Ala Met Ser His Cys Cys Tyr Asn Pro Ile Ile Tyr Cys  
 370 375 380

Tyr Met Asn Ala Arg Phe Arg Ser Gly Phe Val Gln Leu Met His Arg  
 385 390 395 400

Met Pro Gly Leu Arg Arg Trp Cys Cys Leu Arg Ser Val Gly Asp Arg  
 405 410 415

Met Asn Ala Thr Ser Gly Glu Met Thr Thr Lys Tyr His Arg His Val  
 420 425 430

Gly Asp Ala Leu Phe Arg Lys Pro Lys Ile Cys Ile Arg Asn Gly Ser  
 435 440 445

Ser Thr Ser Ser Gln Ser Asn Glu His Ile His His Leu His Gln Arg  
 450 455 460

Ser Ser Lys Ala Thr Ser Asp Ile Phe Ala Ser Glu Pro Ile Ile Met  
 465 470 475 480

Arg Arg Asp Val Thr Thr Ala Val Ala Val Ile Ser Lys Asn Lys Thr  
 485 490 495

Asp Ser Pro Val Arg Arg Ser Gly Ser Ser Gly Gly Thr Glu Ala Asn  
 500 505 510

Ile Arg Ser Thr Glu Phe  
 515

<210> 17

<211> 1628

<212> DNA

<213> D. melanogaster

<400> 17  
 atggcaatgg acttaatcga gcaggagtcc cgcctggaat tcctgcccgg agccgaggag : 60  
 gaagcagaat ttgagcgtct atacgcggct cccgctgaga ttgtggccct gttgtccatt 120  
 ttctatgggg gaatcagtat cgtggccgctc attggcaaca ctttggtcat ctgggtggtg 180

gccacgacca ggcaaatgcg gaccgtgaca aatatgtata tcgctaattt ggcttttggc 240  
gatgtgatta ttggcctctt ctgcatacca ttccagttcc aggctgccct gctgcagagt 300  
tggaacctgc cgtggttcat gtgcagcttc tgccccttcg tccaggccct gagtgtaaat 360  
gtctcgggtat tcacgctgac cgccattgca atcgatcggc atagggccat cattaatcca 420  
cttagggcac gtcccaccaa gttcgtatcg aagttcataa ttggtggaat ttggatgctg 480  
gccctgctat ttgcggtgcc ctttgccatt gcctttcgtg tggaggagt gaccgaaaga 540  
tttcgcgaga acaatgagac ctacaatgtg acgcggccat tctgcatgaa caagaaccta 600  
tccgatgata aattgcaatc ctttcgctac accctggttt ttgtgcagta tctggttcca 660  
ttctgtgtca tcagctttgt ctacatccag atggcggtac gattgtgggg cacacgtgct 720  
cctggtaacg cacaggattc acgggacata acgctgttga aaaacaagaa gaaggtcatc 780  
aaaatgctga ttatcgtggt cattatcttt ggactctgct ggctgccact gcagctctat 840  
aatattctgt atgtcacgat accggaatc aacgactacc acttcattag catcgtctgg 900  
ttttgctgcg attggctggc catgagcaat agctgctaca atccctttat ttatggcatc 960  
tacaatgaaa aatttaagcg ggaattcaac aagcgatttg cggcctgttt ctgcaagttc 1020  
aagacgagca tggacgcca cgaaaggacc ttttcgatgc acaccgcgc cagctccata 1080  
aggtcaacct acgccaactc ctgatgca atccggagta atctctttgg tccggcgct 1140  
gggtggtgtca acaatgggaa gccgggcttg catatgccgc ggtgcatgg atccggtgct 1200  
aacagcggca tttaacaagg aagtagtggg cagaacaaca atgtcaatgg ccaacatcat 1260  
cagcatcaaa gcgtggttac ctttgcggcc actccgggtg tttcggcacc aggtgttggc 1320  
gttgcaatgc cgccgtggcg gcgaaacaac ttcaaacctc tgcattccgaa cgtaatcgaa 1380  
tgcgaggacg acgtggcact catggagctg ccatcaacca cgccccccag cgaggagtgtg 1440  
gcatccgggg ccggagtcca gttggccctg ctaagcagg agagctccag ctgcatttgc 1500  
gaacaggaat ttggcagcca aaccgaatgc gatggcacct gcatactcag cgagggtgtcg 1560  
cgagtccacc tgcccggctc gcaggcgaag gacaaggatg cgggcaagtc cttgtggcaa 1620  
ccacttta 1628

<210> 18

<211> 542

<212> PRT

<213> D. melanogaster

&lt;400&gt; 18

Met Ala Met Asp Leu Ile Glu Gln Glu Ser Arg Leu Glu Phe Leu Pro  
 1 5 10 15

Gly Ala Glu Glu Glu Ala Glu Phe Glu Arg Leu Tyr Ala Ala Pro Ala  
 20 25 30

Glu Ile Val Ala Leu Leu Ser Ile Phe Tyr Gly Gly Ile Ser Ile Val  
 35 40 45

Ala Val Ile Gly Asn Thr Leu Val Ile Trp Val Val Ala Thr Thr Arg  
 50 55 60

Gln Met Arg Thr Val Thr Asn Met Tyr Ile Ala Asn Leu Ala Phe Ala  
 65 70 75 80

Asp Val Ile Ile Gly Leu Phe Cys Ile Pro Phe Gln Phe Gln Ala Ala  
 85 90 95

Leu Leu Gln Ser Trp Asn Leu Pro Trp Phe Met Cys Ser Phe Cys Pro  
 100 105 110

Phe Val Gln Ala Leu Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala  
 115 120 125

Ile Ala Ile Asp Arg His Arg Ala Ile Ile Asn Pro Leu Arg Ala Arg  
 130 135 140

Pro Thr Lys Phe Val Ser Lys Phe Ile Ile Gly Gly Ile Trp Met Leu  
 145 150 155 160

Ala Leu Leu Phe Ala Val Pro Phe Ala Ile Ala Phe Arg Val Glu Glu  
 165 170 175

Leu Thr Glu Arg Phe Arg Glu Asn Asn Glu Thr Tyr Asn Val Thr Arg  
 180 185 190

Pro Phe Cys Met Asn Lys Asn Leu Ser Asp Asp Gln Leu Gln Ser Phe  
 195 200 205

Arg Tyr Thr Leu Val Phe Val Gln Tyr Leu Val Pro Phe Cys Val Ile  
 210 215 220

Ser Phe Val Tyr Ile Gln Met Ala Val Arg Leu Trp Gly Thr Arg Ala

225                                      230                                      235                                      240  
 Pro Gly Asn Ala Gln Asp Ser Arg Asp Ile Thr Leu Leu Lys Asn Lys  
    245                                      250                                      255  
 Lys Lys Val Ile Lys Met Leu Ile Ile Val Val Ile Ile Phe Gly Leu  
    260                                      265                                      270  
 Cys Trp Leu Pro Leu Gln Leu Tyr Asn Ile Leu Tyr Val Thr Ile Pro  
    275                                      280                                      285  
 Glu Ile Asn Asp Tyr His Phe Ile Ser Ile Val Trp Phe Cys Cys Asp  
    290                                      295                                      300  
 Trp Leu Ala Met Ser Asn Ser Cys Tyr Asn Pro Phe Ile Tyr Gly Ile  
    305                                      310                                      315                                      320  
 Tyr Asn Glu Lys Phe Lys Arg Glu Phe Asn Lys Arg Phe Ala Ala Cys  
    325                                      330                                      335  
 Phe Cys Lys Phe Lys Thr Ser Met Asp Ala His Glu Arg Thr Phe Ser  
    340                                      345                                      350  
 Met His Thr Arg Ala Ser Ser Ile Arg Ser Thr Tyr Ala Asn Ser Ser  
    355                                      360                                      365  
 Met Arg Ile Arg Ser Asn Leu Phe Gly Pro Ala Arg Gly Gly Val Asn  
    370                                      375                                      380  
 Asn Gly Lys Pro Gly Leu His Met Pro Arg Val His Gly Ser Gly Ala  
    385                                      390                                      395                                      400  
 Asn Ser Gly Ile Tyr Asn Gly Ser Ser Gly Gln Asn Asn Asn Val Asn  
    405                                      410                                      415  
 Gly Gln His His Gln His Gln Ser Val Val Thr Phe Ala Ala Thr Pro  
    420                                      425                                      430  
 Gly Val Ser Ala Pro Gly Val Gly Val Ala Met Pro Pro Trp Arg Arg  
    435                                      440                                      445  
 Asn Asn Phe Lys Pro Leu His Pro Asn Val Ile Glu Cys Glu Asp Asp  
    450                                      455                                      460  
 Val Ala Leu Met Glu Leu Pro Ser Thr Thr Pro Pro Ser Glu Glu Leu  
    Page 30

465                      470                      475                      480  
 Ala Ser Gly Ala Gly Val Gln Leu Ala Leu Leu Ser Arg Glu Ser Ser  
                                  485                                   490                                   495  
 Ser Cys Ile Cys Glu Gln Glu Phe Gly Ser Gln Thr Glu Cys Asp Gly  
                                  500                                   505                                   510  
 Thr Cys Ile Leu Ser Glu Val Ser Arg Val His Leu Pro Gly Ser Gln  
                                  515                                   520                                   525  
 Ala Lys Asp Lys Asp Ala Gly Lys Ser Leu Trp Gln Pro Leu  
                                  530                                   535                                   540

<210> 19

<211> 1451

<212> DNA

<213> D. melanogaster

<400> 19  
 atgtttacgt ggctgatgat ggatgtcctc cagtttgtga aaggggaaat gacagccgat 60  
 tcagaggcaa atgccacaaa ttggtataac acgaacgaga gcttatatac cacggaactg 120  
 aaccatagat ggattagtgg tagttccaca attcagccag aggagtccct ttatggcact 180  
 gatttgccca cctatcaaca ttgcatagcc acgcggaatt cctttgctga cttgttcact 240  
 gtggtgctct acggatttgt gtgcattatc ggattatttg gcaacaccct ggtgatctac 300  
 gtggtgttgc gctttttcaa aatgcaaacg gtcacgaata tatatatcct gaatctggcg 360  
 gtggcagacg agtgcttcct gattggaata ccttttctgc tgtacacaat gcgaatttgc 420  
 agctggcgat tcggggagtt tatgtgcaaa gcctacatgg tgagcacatc catcacctcc 480  
 ttcacctcgt cgatttttct gctcatcatg tccgcggatc gatatatagc ggtatgccac 540  
 ccgatttcct cgccacgata tcgaactctg catattgccca aagtgggtctc agcgattgcc 600  
 tgggtcaactt cagcggtcct catgctgccc gtgaccttt atgccagcac tgtggagcag 660  
 gaggatggca tcaattactc gtgcaacata atgtggccag atgcgtacaa gaagcattcg 720  
 ggcaccacct tcatactgta cacatttttc ctaggattcg ccacaccgct gtgctttatc 780  
 ctgagtttct actacttggg tataaggaaa ctgcgatcgg tgggtcccaa accaggaacg 840  
 aagtccaagg agaagaggcg ggctcacagg aaggtcactc gactgggtact gacggtgata 900

```

agtgtataca ttctatgttg gctccctcac tggatttctc aggtggccct gattcactcg      960
aatcccgcgcg aaaggggacct ctcccgactg gaaatactca ttttcctact tctggggggca    1020
ctgggtttact cgaattcggc ggtgaatccc atactttatg ccttcctaag tgagaacttc      1080
cggaagagct tcttcaaggc ctttacctgt atgaataagc aggatatcaa cgctcaactc      1140
cagctggagc ccagtgtttt caccaaacag ggcagtaaaa agaggggtgg ctccaagcgc      1200
ctgttgacca gcaatccgca gattcctcca ctgctgccac tgaatgcggg taacaacaat      1260
tcatcgacca ccacatcctc gaccacgaca gcgggaaaaga ccggaaccac ggggacacag      1320
aaatcatgca attccaatgg caaagtgaca gctccgccgg agaatttgat tatatgtttg      1380
agcgagcagc aggaggcatt ttgcaccacc gcgagaagag gatcggggcg agtgcagcag      1440
acagatttgt a                                                                1451

```

&lt;210&gt; 20

&lt;211&gt; 483

&lt;212&gt; PRT

&lt;213&gt; D. melanogaster

&lt;400&gt; 20

```

Met Phe Thr Trp Leu Met Met Asp Val Leu Gln Phe Val Lys Gly Glu
1           5           10           15

```

```

Met Thr Ala Asp Ser Glu Ala Asn Ala Thr Asn Trp Tyr Asn Thr Asn
          20           25           30

```

```

Glu Ser Leu Tyr Thr Thr Glu Leu Asn His Arg Trp Ile Ser Gly Ser
35           40           45

```

```

Ser Thr Ile Gln Pro Glu Glu Ser Leu Tyr Gly Thr Asp Leu Pro Thr
50           55           60

```

```

Tyr Gln His Cys Ile Ala Thr Arg Asn Ser Phe Ala Asp Leu Phe Thr
65           70           75           80

```

```

Val Val Leu Tyr Gly Phe Val Cys Ile Ile Gly Leu Phe Gly Asn Thr
85           90           95

```

```

Leu Val Ile Tyr Val Val Leu Arg Phe Ser Lys Met Gln Thr Val Thr
100          105          110

```



Asn Ile Tyr Ile Leu Asn Leu Ala Val Ala Asp Glu Cys Phe Leu Ile  
 115 120 125

Gly Ile Pro Phe Leu Leu Tyr Thr Met Arg Ile Cys Ser Trp Arg Phe  
 130 135 140

Gly Glu Phe Met Cys Lys Ala Tyr Met Val Ser Thr Ser Ile Thr Ser  
 145 150 155 160

Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala Asp Arg Tyr Ile  
 165 170 175

Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg Thr Leu His Ile  
 180 185 190

Ala Lys Val Val Ser Ala Ile Ala Trp Ser Thr Ser Ala Val Leu Met  
 195 200 205

Leu Pro Val Ile Leu Tyr Ala Ser Thr Val Glu Gln Glu Asp Gly Ile  
 210 215 220

Asn Tyr Ser Cys Asn Ile Met Trp Pro Asp Ala Tyr Lys Lys His Ser  
 225 230 235 240

Gly Thr Thr Phe Ile Leu Tyr Thr Phe Phe Leu Gly Phe Ala Thr Pro  
 245 250 255

Leu Cys Phe Ile Leu Ser Phe Tyr Tyr Leu Val Ile Arg Lys Leu Arg  
 260 265 270

Ser Val Gly Pro Lys Pro Gly Thr Lys Ser Lys Glu Lys Arg Arg Ala  
 275 280 285

His Arg Lys Val Thr Arg Leu Val Leu Thr Val Ile Ser Val Tyr Ile  
 290 295 300

Leu Cys Trp Leu Pro His Trp Ile Ser Gln Val Ala Leu Ile His Ser  
 305 310 315 320

Asn Pro Ala Gln Arg Asp Leu Ser Arg Leu Glu Ile Leu Ile Phe Leu  
 325 330 335

Leu Leu Gly Ala Leu Val Tyr Ser Asn Ser Ala Val Asn Pro Ile Leu  
 340 345 350

Tyr Ala Phe Leu Ser Glu Asn Phe Arg Lys Ser Phe Phe Lys Ala Phe  
 355 360 365

Thr Cys Met Asn Lys Gln Asp Ile Asn Ala Gln Leu Gln Leu Glu Pro  
 370 375 380

Ser Val Phe Thr Lys Gln Gly Ser Lys Lys Arg Gly Gly Ser Lys Arg  
 385 390 395 400

Leu Leu Thr Ser Asn Pro Gln Ile Pro Pro Leu Leu Pro Leu Asn Ala  
 405 410 415

Gly Asn Asn Asn Ser Ser Thr Thr Thr Ser Ser Thr Thr Thr Ala Glu  
 420 425 430

Lys Thr Gly Thr Thr Gly Thr Gln Lys Ser Cys Asn Ser Asn Gly Lys  
 435 440 445

Val Thr Ala Pro Pro Glu Asn Leu Ile Ile Cys Leu Ser Glu Gln Gln  
 450 455 460

Glu Ala Phe Cys Thr Thr Ala Arg Arg Gly Ser Gly Ala Val Gln Gln  
 465 470 475 480

Thr Asp Leu

<210> 21

<211> 1754

<212> DNA

<213> D. melanogaster

<400> 21  
 atgttcaact acgaggaggg g gatgccgac caggcggcca tggctgcagc ggctgcctat 60  
 agggcactgc tcgactacta tgccaatgcg ccaagtgcgg cgggtcacat agtgtcgctc 120  
 aacgtggcac cctacaatgg aactggaaac ggaggcactg tctccttggc gggcaatgcg 180  
 acaagcagct atggcgatga tgatagggat ggctatatgg acaccgagcc cagtgcctg 240  
 gtcaccgaac tggccttctc cctgggcacc agttcaagtc caagtcccag ttccacaccc 300  
 gcttcagct ccagtacttc cactggcatg cccgtctggc tgatacccag ctatagcatg 360

attctgctgt tgcgcgtgct gggcaacctg ctggatcatct cgacgctggt gcagaatcgc 420  
cggatgcgta ccataaccaa cgtgttctctg ctcaacctgg ccataatcga catgctgctg 480  
ggcgtgctct gcatgcccggt caccctgggtg ggcaccctgc tgcgaaactt catctttggc 540  
gagttctctt gcaagctctt tcagttctcg caagccgcct ccgtggccgt ttcgtcctgg 600  
accttggtgg ccataatcctg tgagcgctac tacgcgatat gccatccact gcgctcgcga 660  
tcctggcaga caatcagtcg cgctacaag atcatcggct tcctctggct gggcggcatc 720  
ctctgcatga cgcccatagc ggtcttttagt caattgatac ccaccagtcg accgggctac 780  
tgcaagtgcc gtgagttttg gcccgaccag ggatacgagc tcttctacaa catcctgctg 840  
gacttctctg tgctcgctct gccgcttctc gtcctctgcg tggcctacat cctcatcacg 900  
cgtaccctgt acgtaggcat ggccaaggac agcggacgca tcctgcagca atcgtgcct 960  
gtttccgcta caacggcccg cggaagcgca ccgaatccgg gcaccagcag cagtagtaac 1020  
tgcatcctgg tcctgaccgc caccgcagtc tataatgaaa atagtaacaa taataatgga 1080  
aattcagagg gatccgcagg cggaggatca accaatatgg caacgaccac cttgacaacg 1140  
agaccaacgg ctccaactgt gatcaccacc accacgacga ccacggtgac gctggccaag 1200  
acctcctcgc ccagcattcg cgtccacgat gcggcacttc gcaggtccaa cgaggccaag 1260  
accctggaga gcaagaagcg tgtggtcaag atgctgttcg tcctgggtgct ggagtttttc 1320  
atctgctgga ctccgctgta cgtgatcaac acgatggtca tgctgatcgg accggtggtg 1380  
tacgagtatg tcgactacac ggccatcagt ttccctccagc tgctggccta ctcatccagc 1440  
tgctgcaatc cgatcaccta ctgcttcatg aacgccagct tccggcgcgc ctttgtcgac 1500  
accttcaagg gtctgccctg gcgtcgtgga gcaggtgcca gcggaggcgt cgggtggtgct 1560  
gctggtggag gactctccgc cagccaggcg ggcgcaggcc cgggcgccta tgcgagtgcc 1620  
aacaccaaca ttagtctcaa tcccggccta gccatgggta tgggcacctg gcggagtcgc 1680  
tcacgccacg agtttctcaa tgcggtggtg accaccaata gtgccgccgc cgccgtcaac 1740  
agtcctcagc tcta 1754

<210> 22

<211> 584

<212> PRT

<213> D. melanogaster

<400> 22

Met Phe Asn Tyr Glu Glu Gly Asp Ala Asp Gln Ala Ala Met Ala Ala  
 1 5 10 15  
 Ala Ala Ala Tyr Arg Ala Leu Leu Asp Tyr Tyr Ala Asn Ala Pro Ser  
 20 25 30  
 Ala Ala Gly His Ile Val Ser Leu Asn Val Ala Pro Tyr Asn Gly Thr  
 35 40 45  
 Gly Asn Gly Gly Thr Val Ser Leu Ala Gly Asn Ala Thr Ser Ser Tyr  
 50 55 60  
 Gly Asp Asp Asp Arg Asp Gly Tyr Met Asp Thr Glu Pro Ser Asp Leu  
 65 70 75 80  
 Val Thr Glu Leu Ala Phe Ser Leu Gly Thr Ser Ser Ser Pro Ser Pro  
 85 90 95  
 Ser Ser Thr Pro Ala Ser Ser Ser Ser Thr Ser Thr Gly Met Pro Val  
 100 105 110  
 Trp Leu Ile Pro Ser Tyr Ser Met Ile Leu Leu Phe Ala Val Leu Gly  
 115 120 125  
 Asn Leu Leu Val Ile Ser Thr Leu Val Gln Asn Arg Arg Met Arg Thr  
 130 135 140  
 Ile Thr Asn Val Phe Leu Leu Asn Leu Ala Ile Ser Asp Met Leu Leu  
 145 150 155 160  
 Gly Val Leu Cys Met Pro Val Thr Leu Val Gly Thr Leu Leu Arg Asn  
 165 170 175  
 Phe Ile Phe Gly Glu Phe Leu Cys Lys Leu Phe Gln Phe Ser Gln Ala  
 180 185 190  
 Ala Ser Val Ala Val Ser Ser Trp Thr Leu Val Ala Ile Ser Cys Glu  
 195 200 205  
 Arg Tyr Tyr Ala Ile Cys His Pro Leu Arg Ser Arg Ser Trp Gln Thr  
 210 215 220  
 Ile Ser His Ala Tyr Lys Ile Ile Gly Phe Ile Trp Leu Gly Gly Ile  
 225 230 235 240

Leu Cys Met Thr Pro Ile Ala Val Phe Ser Gln Leu Ile Pro Thr Ser  
 245 250 255

Arg Pro Gly Tyr Cys Lys Cys Arg Glu Phe Trp Pro Asp Gln Gly Tyr  
 260 265 270

Glu Leu Phe Tyr Asn Ile Leu Leu Asp Phe Leu Leu Leu Val Leu Pro  
 275 280 285

Leu Leu Val Leu Cys Val Ala Tyr Ile Leu Ile Thr Arg Thr Leu Tyr  
 290 295 300

Val Gly Met Ala Lys Asp Ser Gly Arg Ile Leu Gln Gln Ser Leu Pro  
 305 310 315 320

Val Ser Ala Thr Thr Ala Gly Gly Ser Ala Pro Asn Pro Gly Thr Ser  
 325 330 335

Ser Ser Ser Asn Cys Ile Leu Val Leu Thr Ala Thr Ala Val Tyr Asn  
 340 345 350

Glu Asn Ser Asn Asn Asn Asn Gly Asn Ser Glu Gly Ser Ala Gly Gly  
 355 360 365

Gly Ser Thr Asn Met Ala Thr Thr Thr Leu Thr Thr Arg Pro Thr Ala  
 370 375 380

Pro Thr Val Ile Thr Thr Thr Thr Thr Thr Thr Val Thr Leu Ala Lys  
 385 390 395 400

Thr Ser Ser Pro Ser Ile Arg Val His Asp Ala Ala Leu Arg Arg Ser  
 405 410 415

Asn Glu Ala Lys Thr Leu Glu Ser Lys Lys Arg Val Val Lys Met Leu  
 420 425 430

Phe Val Leu Val Leu Glu Phe Phe Ile Cys Trp Thr Pro Leu Tyr Val  
 435 440 445

Ile Asn Thr Met Val Met Leu Ile Gly Pro Val Val Tyr Glu Tyr Val  
 450 455 460

Asp Tyr Thr Ala Ile Ser Phe Leu Gln Leu Leu Ala Tyr Ser Ser Ser  
 465 470 475 480

Cys Cys Asn Pro Ile Thr Tyr Cys Phe Met Asn Ala Ser Phe Arg Arg  
 485 490 495

Ala Phe Val Asp Thr Phe Lys Gly Leu Pro Trp Arg Arg Gly Ala Gly  
 500 505 510

Ala Ser Gly Gly Val Gly Gly Ala Ala Gly Gly Gly Leu Ser Ala Ser  
 515 520 525

Gln Ala Gly Ala Gly Pro Gly Ala Tyr Ala Ser Ala Asn Thr Asn Ile  
 530 535 540

Ser Leu Asn Pro Gly Leu Ala Met Gly Met Gly Thr Trp Arg Ser Arg  
 545 550 555 560

Ser Arg His Glu Phe Leu Asn Ala Val Val Thr Thr Asn Ser Ala Ala  
 565 570 575

Ala Ala Val Asn Ser Pro Gln Leu  
 580

<210> 23

<211> 1452

<212> DNA

<213> D. melanogaster

<400> 23  
 atgtacgcct ccttgatgga cgttggccag acgttggcag ccaggctggc ggatagcgac 60  
 ggcaacgggg ccaatgacag cggactcctg gcaaccggac aaggtctgga gcaggagcag 120  
 gagggctctgg cactggatat gggccacaat gccagcgccg acggcggaat agtaccgtat 180  
 gtgcccgtgc tggaccgccc ggagacgtac attgtcaccg tgctgtacac gtcacatctc 240  
 attgtgggag ttttgggcaa cggcacgctg gtcacatctt tctttcgcca ccgtccatg 300  
 cgcaacatac ccaacacata cattctttca ctggccctgg ctgatctggt gggttatattg 360  
 gtgtgtgtac ctgtggccac gattgtctac acgcaggaaa gctggccctt tgagcggaac 420  
 atgtgccgca tcagcgagtt cttaaggac atatccatcg ggggtgtccgt gtttacactg 480  
 accgcccttt ccggcgagcg gtactgcgcc attgtaaatc ccctacgcaa gcttcagacc 540  
 aagccgctca ctgtctttac tgcggtgatg atctggatcc tggccatcct actgggcatg 600

ccttcggttc ttttctccga catcaagtcc taccctgtgt tcacagccac cggtaacatg 660  
 accattgaag tgtgctcccc atttcgagac ccggagtatg caaagttcat ggtggcgggc 720  
 aaggcactgg tgtactacct gttgccgctg tccatcattg gggcgctata catcatgatg 780  
 gccaaagcggc tccatatgag cgcccgcaac atgcccgggc aacagcagag catgcagagc 840  
 cgcacccagg ctagggcccg actccatgtg gcgcgcatgg tggtagcatt cgtggtggtg 900  
 ttcttcatct gcttcttccc gtaccacgtg tttagactgt ggtaccactt ctacccaacg 960  
 gctgaggagg acttcgatga gttctggaac gtgctgcgca tccttcctaa actcgtgcgt 1020  
 caaccccggtg gcctctactg cgtgtccggg gtgtttcggc agcactttaa tcgctacctc 1080  
 tgctgcatct gcgtcaagcg gcagccgcac ctgcggcagc actcaacggc cactggaatg 1140  
 atggacaata ccagtgtgat gtccatgcgc cgctccacgt acgtgggtgg aaccgctggc 1200  
 aatctgcggg cctcgctgca ccggaacagc aatcacggag ttggtggagc tggaggtgga 1260  
 gtaggaggag gagtagggtc aggtcgtgtg ggcagctttc atcggcagga ctcgatgcc 1320  
 ctgcagcacg gaaatgccca cggaggtggt gcgggcgggg gatcctccgg acttgagacc 1380  
 ggcgggcgga cggcggcagt gagcgaaaag agctttataa atcgttacga aagtggcgta 1440  
 atgcgctact aa 1452

<210> 24

<211> 483

<212> PRT

<213> D. melanogaster

<400> 24

Met Tyr Ala Ser Leu Met Asp Val Gly Gln Thr Leu Ala Ala Arg Leu  
 1 5 10 15

Ala Asp Ser Asp Gly Asn Gly Ala Asn Asp Ser Gly Leu Leu Ala Thr  
 20 25 30

Gly Gln Gly Leu Glu Gln Glu Gln Glu Gly Leu Ala Leu Asp Met Gly  
 35 40 45

His Asn Ala Ser Ala Asp Gly Gly Ile Val Pro Tyr Val Pro Val Leu  
 50 55 60

Asp Arg Pro Glu Thr Tyr Ile Val Thr Val Leu Tyr Thr Leu Ile Phe

Page 40



305                      310                      315                      320  
 Ala Glu Glu Asp Phe Asp Glu Phe Trp Asn Val Leu Arg Ile Leu Pro  
                                  325                                   330                                   335  
 Lys Leu Val Arg Gln Pro Arg Gly Leu Tyr Cys Val Ser Gly Val Phe  
                                  340                                   345                                   350  
 Arg Gln His Phe Asn Arg Tyr Leu Cys Cys Ile Cys Val Lys Arg Gln  
                                  355                                   360                                   365  
 Pro His Leu Arg Gln His Ser Thr Ala Thr Gly Met Met Asp Asn Thr  
                                  370                                   375                                   380  
 Ser Val Met Ser Met Arg Arg Ser Thr Tyr Val Gly Gly Thr Ala Gly  
                                  385                                   390                                   395                                   400  
 Asn Leu Arg Ala Ser Leu His Arg Asn Ser Asn His Gly Val Gly Gly  
                                  405                                   410                                   415  
 Ala Gly Gly Gly Val Gly Gly Gly Val Gly Ser Gly Arg Val Gly Ser  
                                  420                                   425                                   430  
 Phe His Arg Gln Asp Ser Met Pro Leu Gln His Gly Asn Ala His Gly  
                                  435                                   440                                   445  
 Gly Gly Ala Gly Gly Gly Ser Ser Gly Leu Gly Ala Gly Gly Arg Thr  
                                  450                                   455                                   460  
 Ala Ala Val Ser Glu Lys Ser Phe Ile Asn Arg Tyr Glu Ser Gly Val  
                                  465                                   470                                   475                                   480  
 Met Arg Tyr

&lt;210&gt; 25

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Novel Sequence

<400> 25

Thr Asp Val Asp His Val Phe Leu Arg Phe  
1 5 10

<210> 26

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 26

Asp Pro Lys Gln Asp Phe Met Arg Phe  
1 5

<210> 27

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 27

Pro Asp Asn Phe Met Arg Phe  
1 5

<210> 28

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 28

Thr Pro Ala Glu Asp Phe Met Arg Phe  
1 5

<210> 29

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 29

Ser Leu Lys Gln Asp Phe Met His Phe  
1 5

<210> 30

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 30

Ser Val Lys Gln Asp Phe Met His Phe  
1 5

<210> 31

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 31

Ala Ala Met Asp Arg Tyr  
1 5

<210> 32

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 32

Ser Val Gln Asp Asn Phe Met His Phe  
1 5

<210> 33

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 33

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe  
1 5 10

<210> 34

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 34

Gly Asp Gly Arg Leu Tyr Ala Phe Gly Leu  
1 5 10

<210> 35

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 35

Asp Arg Leu Tyr Ser Phe Gly Leu  
1 5

<210> 36

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 36

Ala Pro Ser Gly Ala Gln Arg Leu Tyr Gly Phe Gly Leu  
1 5 10

<210> 37

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 37

Gly Gly Ser Leu Tyr Ser Phe Gly Leu  
1 5

<210> 38

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 38

Phe Ile Arg Phe  
1

<210> 39

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 39

Lys Asn Glu Phe Ile Arg Phe  
1 5

<210> 40

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 40

Phe Met Arg Phe  
1

<210> 41

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 41

Lys Ser Ala Phe Met Arg Phe  
1 5

<210> 42

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 42

Lys Pro Asn Phe Leu Arg Phe  
1 5

<210> 43

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 43

Phe Leu Arg Phe  
1

<210> 44

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 44

Tyr Leu Arg Phe  
1

<210> 45

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 45

Lys Pro Asn Phe Leu Arg Tyr  
1 5

<210> 46

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence



<400> 46

Thr Asn Arg Asn Phe Leu Arg Phe  
1 5

<210> 47

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 47

Arg Asn Lys Phe Glu Phe Ile Arg Phe  
1 5

<210> 48

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 48

Ala Gly Pro Arg Phe Ile Arg Phe  
1 5

<210> 49

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 49

Gly Leu Gly Pro Arg Pro Leu Arg Phe  
1 5

<210> 50

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 50

Ile Leu  
1

<210> 51

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 51

Ala Gly Ala Lys Ile Phe Arg Phe  
1 5

<210> 52

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 52

Ala Pro Lys Pro Lys Phe Ile Arg Phe  
1 5

<210> 53

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 53

Lys Ser Ala Phe Val Leu Arg Phe  
1 5

<210> 54

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 54

Thr Lys Phe Gln Asp Phe Leu Arg Phe  
1 5

<210> 55

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 55

Ser Ala Glu Pro Phe Gly Thr Met Arg Phe  
1 5 10

<210> 56

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 56

Ala Ser Glu Asp Ala Leu Phe Gly Thr Met Arg Phe  
1 5 10

<210> 57

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 57

Ser Ala Asp Asp Ser Ala Pro Phe Gly Thr Met Arg Phe  
1 5 10

<210> 58

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 58

Glu Asp Gly Asn Ala Pro Phe Gly Thr Met Arg Phe  
1 5 10

<210> 59

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 59

Phe Leu Phe Gln Pro Gln Arg Phe  
1 5

<210> 60

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 60

Ser Ala Asp Pro Asn Phe Leu Arg Phe  
1 5

<210> 61

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 61

Ser Gln Pro Asn Phe Leu Arg Phe  
1 5

<210> 62

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 62

Ala Ser Gly Asp Pro Asn Phe Leu Arg Phe  
1 5 10

<210> 63

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 63

Ser Asp Pro Asn Phe Leu Arg Phe  
1 5

<210> 64

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 64

Ala Ala Ala Asp Pro Asn Phe Leu Arg Phe  
1. 5 10

<210> 65

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 65

Pro Asn Phe Leu Arg Phe  
1 5

<210> 66

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 66

Lys Pro Phe Leu Arg Phe  
1 5

<210> 67

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 67

Ala Gly Ser Asp Pro Asn Phe Leu Arg Phe  
1 5 10

<210> 68

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 68

Lys Pro Asn Phe Leu Arg Tyr  
1 5

<210> 69

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 69

Ser Pro Arg Glu Pro Ile Arg Phe  
1 5

<210> 70

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence



<400> 70

Leu Arg Gly Glu Pro Ile Arg Phe  
1 5

<210> 71

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 71

Ser Pro Leu Gly Thr Met Arg Phe  
1 5

<210> 72

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 72

Glu Ala Glu Glu Pro Leu Gly Thr Met Arg Phe  
1 5 10

<210> 73

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 73

Ala Ser Glu Asp Ala Leu Phe Gly Thr Met Arg Phe  
1 5 10

<210> 74

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 74

Glu Asp Gly Asn Ala Pro Phe Gly Thr Met Arg Phe  
1 5 10

<210> 75

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 75

Ser Ala Glu Pro Phe Gly Thr Met Arg Phe  
1 5 10

<210> 76

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 76

Ser Ala Asp Asp Ser Ala Pro Phe Gly Thr Met Arg Phe  
1 5 10

<210> 77

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 77

Lys Pro Thr Phe Ile Arg Phe  
1 5

<210> 78

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 78

Ala Ser Pro Ser Phe Ile Arg Phe  
1 5

<210> 79

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 79

Gly Ala Lys Phe Ile Arg Phe  
1 5

<210> 80

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 80

Ala Gly Ala Lys Phe Ile Arg Phe  
1 5

<210> 81

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 81

Ala Pro Lys Pro Lys Phe Ile Arg Phe  
1 5

<210> 82

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 82

Lys Ser Ala Tyr Met Arg Phe  
1 5

<210> 83

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 83

Ser Pro Met Gln Arg Ser Ser Met Val Arg Phe  
1 5 10

<210> 84

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 84

Ser Pro Met Glu Arg Ser Ala Met Val Arg Phe  
1 5 10

<210> 85

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 85

Ser Pro Met Asp Arg Ser Lys Met Val Arg Phe  
1 5 10

<210> 86

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 86

Lys Asn Glu Phe Ile Arg Phe  
1 5

<210> 87

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 87

Lys Pro Ser Phe Val Arg Phe  
1 5

<210> 88

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 88

Gln Pro Lys Ala Arg Ser Gly Tyr Ile Arg Phe  
1 5 10

<210> 89

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 89

Ala Met Arg Asn Ala Leu Val Arg Phe  
1 5

<210> 90

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 90

Ala Ser Gly Gly Met Arg Asn Ala Leu Val Arg Phe  
1 5 10

<210> 91

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 91

Asn Gly Ala Pro Gln Pro Phe Val Arg Phe  
1 5 10

<210> 92

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 92

Arg Asn Lys Phe Glu Phe Ile Arg Phe  
1 5

<210> 93

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 93

Ser Asp Arg Pro Thr Arg Ala Met Asp Ser Pro Ile Arg Phe  
1 5 10

<210> 94

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence



400> 94

Ia Ala Asp Gly Ala Pro Leu Ile Arg Phe  
5 10

210> 95

211> 10

212> PRT

213> Artificial Sequence

220>

223> Novel Sequence

400> 95

Ia Pro Glu Ala Ser Pro Phe Ile Arg Phe  
5 10

210> 96

211> 10

212> PRT

213> Artificial Sequence

220>

223> Novel Sequence

400> 96

Ia Ser Pro Ser Ala Pro Leu Ile Arg Phe  
5 10

210> 97

211> 10

212> PRT

213> Artificial Sequence

220>

223> Novel Sequence

<400> 100

Ser Leu Asp Tyr Arg Phe  
1 5

<210> 101

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 101

Glu Ile Val Phe His Gln Ile Ser Pro Ile Phe Phe Arg Phe  
1 5 10

<210> 102

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 102

Gly Gly Pro Gln Gly Pro Leu Arg Phe  
1 5

<210> 103

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 103

Gly Pro Ser Gly Pro Leu Arg Phe  
1 5

<210> 104

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 104

Ala Gln Thr Phe Val Arg Phe  
1 5

<210> 105

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 105

Gly Gln Thr Phe Val Arg Phe  
1 5

<210> 106

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 106 .

Lys Ser Ala Phe Val Arg Phe  
1 5

<210> 107

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 107

Lys Ser Gln Tyr Ile Arg Phe  
1 5

<210> 108

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 108

Asp Val Pro Gly Val Leu Arg Phe  
1 5

<210> 109

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 109

Lys Ser Val Pro Gly Val Leu Arg Phe  
1 5

<210> 110

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 110

Ser Glu Val Pro Gly Val Leu Arg Phe  
1 5

<210> 111

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 111

Ser Val Pro Gly Val Leu Arg Phe  
1 5

<210> 112

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 112

Asp Phe Asp Gly Ala Met Pro Gly Val Leu Arg Phe  
1 5 10

<210> 113

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 113

Glu Ile Pro Gly Val Leu Arg Phe  
1 5

<210> 114

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 114

Trp Ala Asn Gln Val Arg Phe  
1 5

<210> 115

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 115

Ala Ser Trp Ala Ser Ser Val Arg Phe  
1 5

<210> 116

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 116

Ala Met Met Arg Phe  
1 5

<210> 117

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 117

Gly Leu Gly Pro Arg Pro Leu Arg Phe  
1 5

<210> 118

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 118

Ser Pro Ser Ala Lys Trp Met Arg Phe  
1 5

<210> 119

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 119

Thr Lys Phe Gln Asp Phe Leu Arg Phe  
1 5

<210> 120

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 120

Glu Asp Arg Asp Tyr Arg Pro Leu Gln Phe  
1 5 10

<210> 121

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence



<400> 121

Phe Ile Arg Phe  
1

<210> 122

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 122

Ala Val Pro Gly Val Leu Arg Phe  
1 5

<210> 123

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 123

Gly Asp Val Pro Gly Val Leu Arg Phe  
1 5

<210> 124

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 124

Ser Asp Ile Gly Ile Ser Glu Pro Asn Phe Leu Arg Phe  
1 5 10

<210> 125

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 125

Ser Gly Lys Pro Thr Phe Ile Arg Phe  
1 5

<210> 126

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 126

Ala Glu Gly Leu Ser Ser Pro Leu Ile Arg Phe  
1 5 10

<210> 127

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 127

Phe Asp Arg Asp Phe Met Arg Phe  
1 5

<210> 128

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 128

Ala Gly Pro Arg Phe Ile Arg Phe  
1 5

<210> 129

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 129

Gly Met Pro Gly Val Leu Arg Phe  
1 5

<210> 130

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 130

Ile Leu  
1

<210> 131

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 131

Leu Gln Pro Asn Phe Leu Arg Phe  
1 5

<210> 132

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 132

Lys Pro Asn Phe Ile Arg Phe  
1 5

<210> 133

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 133

Phe Met Arg Phe  
1

<210> 134

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 134

Phe Leu Arg Phe  
1

<210> 135

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 135

Tyr Ile Arg Phe  
1

<210> 136

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 136

Gly Asn Ser Phe Leu Arg Phe  
1 5

<210> 137

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 137

Asp Pro Ser Phe Leu Arg Phe  
1 5

<210> 138

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 138

Gln Asp Phe Met Arg Phe  
1 5

<210> 139

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 139

Lys Pro Asn Gln Asp Phe Met Arg Phe  
1 5

<210> 140

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 140

Thr Asp Val Asp His Val Phe Leu Arg Phe  
1 5 10

<210> 141

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 141

Ala Ala Met Asp Arg Tyr  
1 5

<210> 142

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 142

Ser Pro Lys Gln Asp Phe Met Arg Phe  
1 5

<210> 143

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 143

Pro Asp Asn Phe Met Arg Phe  
1 5

<210> 144

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 144

Asp Pro Lys Gln Asp Phe Met Arg Phe  
1 5

<210> 145

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence



<400> 145

Thr Pro Ala Glu Asp Phe Met Arg Phe  
1 5

<210> 146

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 146

Ser Asp Asn Phe Met Arg Phe  
1 5

<210> 147

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 147

Tyr Leu Arg Phe  
1

<210> 148

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 148

Ser Asp Arg Asn Phe Leu Arg Phe  
1 5

<210> 149

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 149

Thr Asn Arg Asn Phe Leu Arg Phe  
1 5

<210> 150

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 150

Pro Asp Val Asp His Val Phe Leu Arg Phe  
1 5 10

<210> 151

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 151

Gln Asp Val Asp His Val Phe Leu Arg Phe  
1 5 10

<210> 152

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 152

Phe Leu Phe Gln Pro Gln Arg Phe  
1 5

<210> 153

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 153

Ala Arg Gly Pro Gln Leu Arg Leu Arg Phe  
1 5 10

<210> 154

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 154

Phe Asp Asp Tyr Gly His Leu Arg Phe  
1 5

<210> 155

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 155

Phe Asp Asp Tyr Gly His Leu Arg Phe  
1 5

<210> 156

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 156

Met Asp Ser Asn Phe Ile Arg Phe  
1 5

<210> 157

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 157

Phe Asp Asp Tyr Gly His Leu Arg Phe  
1 5

<210> 158

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 158

Phe Asp Asp Tyr Gly His Leu Arg Phe  
1 5

<210> 159

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 159

Phe Asp Asp Tyr Gly His Met Arg Phe  
1 5

<210> 160

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

~~<400>~~ 160

Gly Gly Asp Asp Gln Phe Asp Asp Tyr Gly His Met Arg Phe  
1 5 10

<210> 161

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 161

Ser Arg Pro Tyr Ser Phe Gly Leu  
1 5

<210> 162

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 162

Asp Tyr Gly His Met Arg Phe  
1 5

<210> 163

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 163

Ala Pro Arg Thr Pro Gly Gly Arg Arg  
1 5

<210> 164

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 164

Val Glu Arg Tyr Ala Phe Gly Leu  
1 5

<210> 165

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 165

Leu Pro Val Tyr Asn Phe Gly Leu  
1 5

<210> 166

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 166

Thr Thr Arg Pro Gln Pro Phe Asn Phe Gly Leu  
1 5 10

<210> 167

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 167

Glu Asp Val Asp His Val Phe Leu Arg Phe  
1 5 10

<210> 168

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 168

Gly Asn Ser Phe Leu Arg Phe  
1 5

<210> 169

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 169

Ala Pro Thr Ser Ser Phe Ile Gly Met Arg  
1 5 10



<210> 170  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 170

Ala Pro Leu Ala Phe Tyr Gly Met Arg  
1 5

<210> 171  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 171

Ala Pro Leu Ala Phe Tyr Gly Leu Arg  
1 5

<210> 172  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 172

Ala Pro Thr Gly Phe Thr Gly Met Arg  
1 5

<210> 173  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 173

Ala Pro Val Asn Ser Phe Val Gly Met Arg  
1 5 10

<210> 174  
<211> 9  
<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 174

Ala Pro Asn Gly Phe Leu Gly Met Arg  
1 5

<210> 175

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 175

Asp Pro Ala Phe Asn Ser Trp Gly  
1 5

<210> 176

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 176

Gly Ser Gly Phe Ser Ser Trp Gly  
1 5

<210> 177

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> Residue at position 1 is pGlu.

<400> 177

Xaa Ser Ser Phe His Ser Trp Gly  
1 5

<210> 178

<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 178

Gly Ala Ser Phe Tyr Ser Trp Gly  
1 5

<210> 179  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 179

Asn Pro Phe His Ser Trp Gly  
1 5

<210> 180  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 180

Pro Ser Phe His Ser Trp Ser  
1 5

<210> 181  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Novel Sequence

<400> 181

Asn Ser Val Val Leu Gly Lys Lys Gln Arg Phe His Ser Trp Gly  
1 5 10 15

<210> 182  
<211> 15  
<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> Xaa is pGlu.

<400> 182

Xaa	Val	Arg	Phe	Arg	Gln	Cys	Tyr	Phe	Asn	Pro	Ile	Ser	Cys	Phe
1				5					10					15

<210> 183

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<400> 183

Gln	Arg	Phe	His	Ser	Trp	Gly
1				5		

<210> 184

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Novel Sequence

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> Xaa is pGlu

<221> DISULFID

<222> (7)..(14)

<400> 184

Xaa	Val	Arg	Phe	Gln	Cys	Tyr	Phe	Asn	Pro	Ile	Ser	Cys	Phe
1				5					10				

<210> 185

<211> 15

<212> PRT

<213> Artificial Sequence

<220>